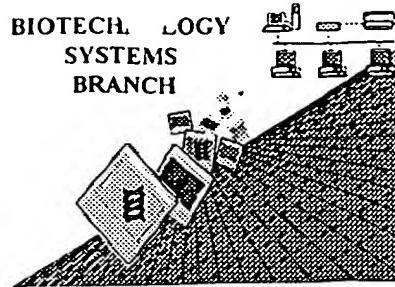


BEST AVAILABLE COPY



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

RECEIVED

Application Serial Number: 09/489,198

JUL 09 2001

Source: 1646

TECH CENTER 1600/2900

Date Processed by STIC: 6-14-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/489, 198

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

#10
Lmey
1-9-01
1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/489,198

DATE: 06/14/2001
TIME: 10:13:12

Input Set : A:\Sequence.txt
Output Set: N:\CRF3\06142001\I489198.raw

3 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA.
 5 <120> TITLE OF INVENTION: Gene screening method using nuclear receptor
 7 <130> FILE REFERENCE: C1-901PCT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/489,198
 C--> 10 <141> CURRENT FILING DATE: 2000-01-20
 12 <150> PRIOR APPLICATION NUMBER: JP 09/212624
 W--> 13 <151> PRIOR FILING DATE: 1997-7-22 → 1997-07-22
 15 <160> NUMBER OF SEQ ID NOS: 4
 17 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
Corrected Diskette Needed
See pp. 1, 2, 5

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1 Valid <212> responses:
 20 <211> LENGTH: 507
 E--> 21 <212> TYPE: RPT - DNA
 22 <213> ORGANISM: Mus musculus - RNA
 24 <400> SEQUENCE: 1 - PRT
 25 Met Thr Gln Ala Val Lys Leu Ala
 26 1 5
 27 Ser Arg Val Phe His Arg Ile His Leu Pro Leu Gln Leu Asp Ala Ser
 28 10 15 20
 29 Leu Gly Ser Arg Gly Ser Glu Ser Val Leu Arg Ser Leu Ser Asp Ile
 30 25 30 35 40
 31 Pro Gly Pro Ser Thr Leu Ser Phe Leu Ala Glu Leu Phe Cys Lys Gly
 32 45 50 55
 33 Gly Leu Ser Arg Leu His Glu Leu Gln Val His Gly Ala Ala Arg Tyr
 34 60 65 70
 35 Gly Pro Ile Trp Ser Gly Ser Phe Gly Thr Leu Arg Thr Val Tyr Val
 36 75 80 85
 37 Ala Asp Pro Thr Leu Val Glu Gln Leu Leu Arg Gln Glu Ser His Cys
 38 90 95 100
 39 Pro Glu Arg Cys Ser Phe Ser Ser Trp Ala Glu His Arg Arg Arg His
 40 105 110 115 120
 41 Gln Arg Ala Cys Gly Leu Leu Thr Ala Asp Gly Glu Glu Trp Gln Arg
 42 125 130 135
 43 Leu Arg Ser Leu Leu Ala Pro Leu Leu Arg Pro Gln Ala Ala Ala
 44 140 145 150
 45 Gly Tyr Ala Gly Thr Leu Asp Asn Val Val Arg Asp Leu Val Arg Arg
 46 155 160 165
 47 Leu Arg Arg Gln Arg Gly Arg Gly Ser Gly Leu Pro Gly Leu Val Leu
 48 170 175 180
 49 Asp Val Ala Gly Glu Phe Tyr Lys Phe Gly Leu Glu Ser Ile Gly Ala
 50 185 190 195 200
 51 Val Leu Leu Gly Ser Arg Leu Gly Cys Leu Glu Ala Glu Val Pro Pro
 52 205 210 215
 53 Asp Thr Glu Thr Phe Ile His Ala Val Gly Ser Val Phe Val Ser Thr

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/489,198

DATE: 06/14/2001
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Input Set : A:\Sequence.txt
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54	220	225	230
55	Leu Leu Thr Met Ala Met Pro Asn Trp Leu His His Leu Ile Pro Gly		
56	235	240	245
57	Pro Trp Ala Arg Leu Cys Arg Asp Trp Asp Gln Met Phe Ala Phe Ala		
58	250	255	260
59	Gln Arg His Val Glu Leu Arg Glu Gly Glu Ala Ala Met Arg Asn Gln		
60	265	270	275
61	Gly Lys Pro Glu Glu Asp Met Pro Ser Gly His His Leu Thr His Phe		
62	285	290	295
63	Leu Phe Arg Glu Lys Val Ser Val Gln Ser Ile Val Gly Asn Val Thr		
64	300	305	310
65	Glu Leu Leu Leu Ala Gly Val Asp Thr Val Ser Asn Thr Leu Ser Trp		
66	315	320	325
67	Thr Leu Tyr Glu Leu Ser Arg His Pro Asp Val Gln Thr Ala Leu His		
68	330	335	340
69	Ser Glu Ile Thr Ala Gly Thr Arg Gly Ser Cys Ala His Pro His Gly		
70	345	350	355
71	70 Thr Ala Leu Ser Gln Leu Pro Leu Leu Lys Ala Val Ile Lys Glu Val		
72	365	370	375
73	Leu Arg Leu Tyr Pro Val Val Pro Gly Asn Ser Arg Val Pro Asp Arg		
74	380	385	390
75	Asp Ile Arg Val Gly Asn Tyr Val Ile Pro Gln Asp Thr Leu Val Ser		
76	395	400	405
77	Leu Cys His Tyr Ala Thr Ser Arg Asp Pro Thr Gln Phe Pro Asp Pro		
78	410	415	420
79	Asn Ser Phe Asn Pro Ala Arg Trp Leu Gly Glu Gly Pro Thr Pro His		
80	425	430	435
81	440		
82	Pro Phe Ala Ser Leu Pro Phe Gly Phe Gly Lys Arg Ser Cys Ile Gly		
83	445	450	455
84	Arg Arg Leu Ala Glu Leu Glu Leu Gln Met Ala Leu Ser Gln Ile Leu		
85	460	465	470
86	475	480	485
87	Thr His Phe Glu Val Leu Pro Glu Pro Gly Ala Leu Pro Ile Lys Pro		
88	490	495	500
89	Met Thr Arg Thr Val Leu Val Pro Glu Arg Ser Ile Asn Leu Gln Phe		
90	505		
92	<210> SEQ ID NO: 2		
93	<211> LENGTH: 508		
E-->	94 <212> TYPE: RPT	Valid response.	
		- DNA	
		- RNA	
		- PRT	
95	<213> ORGANISM: Homo sapiens		
97	<400> SEQUENCE: 2		
98	Met Thr Gln Thr Leu Lys Tyr Ala Ser Arg Val Phe His Arg Val Arg		
99	1	5	10
			15
100	Trp Ala Pro Glu Leu Gly Ala Ser Leu Gly Tyr Arg Glu Tyr His Ser		
101	20	25	30
102	Ala Arg Arg Ser Leu Ala Asp Ile Pro Gly Pro Ser Thr Pro Ser Phe		
103	35	40	45
104	Leu Ala Glu Leu Phe Cys Lys Gly Gly Leu Ser Arg Leu His Glu Leu		

file:///C:/CRF3/Outhold/VsrI489198.htm 6/14/01

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/489,198

DATE: 06/14/2001
TIME: 10:13:12

Input Set : A:\Sequence.txt
Output Set: N:\CRF3\06142001\I489198.raw

105	50	55	60
106	Gln Val Gln Gly Ala Ala His Phe Gly Pro Val Trp Leu Ala Ser Phe		
107	65	70	75
108	Gly Thr Val Arg Thr Val Tyr Val Ala Ala Pro Ala Leu Val Glu Glu		80
109		85	90
110	Leu Leu Arg Gln Glu Gly Pro Arg Pro Glu Arg Cys Ser Phe Ser Pro		95
111		100	105
112	Trp Thr Glu His Arg Arg Cys Arg Gln Arg Ala Cys Gly Leu Leu Thr		110
113		115	120
114	Ala Glu Gly Glu Glu Trp Gln Arg Leu Arg Ser Leu Leu Ala Pro Leu		125
115		130	135
116	Leu Leu Arg Pro Gln Ala Ala Ala Arg Tyr Ala Gly Thr Leu Asn Asn		140
117		145	150
118	Val Val Cys Asp Leu Val Arg Arg Leu Arg Arg Gln Arg Gly Arg Gly		155
119		165	170
120	Thr Gly Pro Pro Ala Leu Val Arg Asp Val Ala Gly Glu Phe Tyr Lys		175
121		180	185
122	Phe Gly Leu Glu Gly Ile Ala Ala Val Leu Leu Gly Ser Arg Leu Gly		190
123		195	200
124	Cys Leu Glu Ala Gln Val Pro Pro Asp Thr Glu Thr Phe Ile Arg Ala		205
125		210	215
126	Val Gly Ser Val Phe Val Ser Thr Leu Leu Thr Met Ala Met Pro His		220
127		225	230
128	Trp Leu Arg His Leu Val Pro Gly Pro Trp Gly Arg Leu Cys Arg Asp		235
129		245	250
130	Trp Asp Gln Met Phe Ala Phe Ala Gln Arg His Val Glu Arg Arg Glu		255
131		260	265
132	Ala Glu Ala Ala Met Arg Asn Gly Gly Gln Pro Glu Lys Asp Leu Glu		270
133		275	280
134	Ser Gly Ala His Leu Thr His Phe Leu Phe Arg Glu Glu Leu Pro Ala		285
135		290	295
136	Gln Ser Ile Leu Gly Asn Val Thr Glu Leu Leu Ala Gly Val Asp		300
137		305	310
138	Thr Val Ser Asn Thr Leu Ser Trp Ala Leu Tyr Glu Leu Ser Arg His		315
139		325	330
140	Pro Glu Val Gln Thr Ala Leu His Ser Glu Ile Thr Ala Ala Leu Ser		335
141		340	345
142	Pro Gly Ser Ser Ala Tyr Pro Ser Ala Thr Val Leu Ser Gln Leu Pro		350
143		355	360
144	Leu Leu Lys Ala Val Val Lys Glu Val Leu Arg Leu Tyr Pro Val Val		365
145		370	375
146	Pro Gly Asn Ser Arg Val Pro Asp Lys Asp Ile His Val Gly Asp Tyr		380
147		385	390
148	Ile Ile Pro Lys Asn Thr Leu Val Thr Leu Cys His Tyr Ala Thr Ser		395
149		405	410
150	Arg Asp Pro Ala Gln Phe Pro Glu Pro Asn Ser Phe Arg Pro Ala Arg		400
151		420	425
152	Trp Leu Gly Glu Gly Pro Thr Pro His Pro Phe Ala Ser Leu Pro Phe		430
153		435	440
			445

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/489,198

DATE: 06/14/2001
TIME: 10:13:12

Input Set : A:\Sequence.txt
Output Set: N:\CRF3\06142001\I489198.raw

154 Gly Phe Gly Lys Arg Ser Cys Met Gly Arg Arg Leu Ala Glu Leu Glu
155 450 455 460
156 Leu Gln Met Ala Leu Ala Gln Ile Leu Thr His Phe Glu Val Gln Pro
157 465 470 475 480
158 Glu Pro Gly Ala Ala Pro Val Arg Pro Lys Thr Arg Thr Val Leu Val
159 485 490 495
160 Pro Glu Arg Ser Ile Asn Leu Gln Phe Leu Asp Arg
161 500 505

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p. 5

<210> 4 Seg. # 4

<211> 2362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1524)

There is an "n" at position 1926
in sequence # 4. It is mandatory
to have <220> to <223> features to
explain what the "n" represents.

See # 9 on the Error Summary
Sheet.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/489,198

DATE: 06/14/2001

TIME: 10:13:13

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\06142001\I489198.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:21 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:94 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:399 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4